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RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/301,380

DATE: 05/10/1999  
TIME: 17:01:02

Input Set: I301380.RAW

This Raw Listing contains the General Information  
Section and up to first 5 pages.

ENTERED

1 <110> APPLICANT: Murphy, Gerald P.  
2 Boynton, Alton L.  
3 Sehgal, Anil  
4 <120> TITLE OF INVENTION: Nr-CAM GENE, NUCLEIC ACIDS AND NUCLEIC ACID PRODUCTS  
5 FOR THERAPEUTIC AND DIAGNOSTIC USES FOR TUMORS  
6 <130> FILE REFERENCE: 8511-021  
7 <140> CURRENT APPLICATION NUMBER: US/09/301,380  
8 <141> CURRENT FILING DATE: 1999-04-27  
9 <150> EARLIER APPLICATION NUMBER: 60/112,098  
10 <151> EARLIER FILING DATE: 1998-12-14  
11 <150> EARLIER APPLICATION NUMBER: 60/083,152  
12 <151> EARLIER FILING DATE: 1998-04-27  
13 <160> NUMBER OF SEQ ID NOS: 32  
14 <170> SOFTWARE: PatentIn Ver. 2.0  
15 <210> SEQ ID NO 1  
16 <211> LENGTH: 4134  
17 <212> TYPE: DNA  
18 <213> ORGANISM: Homo sapiens  
19 <220> FEATURE:  
20 <221> NAME/KEY: CDS  
21 <222> LOCATION: (130)..(4029)  
22 <400> SEQUENCE: 1  
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25 cttaaaata atg ccg aaa aag aag cgc tta tct gcg ggc aga gtg ccc ctg 171  
26 Met Pro Lys Lys Lys Arg Leu Ser Ala Gly Arg Val Pro Leu  
27 1 5 10  
28 att ctc ttc ctg tgc cag atg att agt gca ctg gaa gta cct ctt gat 219  
29 Ile Leu Phe Leu Cys Gln Met Ile Ser Ala Leu Glu Val Pro Leu Asp  
30 15 20 25 30  
31 cca aaa ctt ctt gaa gac ttg gta cag cct cca acc atc acc caa cag 267  
32 Pro Lys Leu Leu Glu Asp Leu Val Gln Pro Pro Thr Ile Thr Gln Gln  
33 35 40 45  
34 tct cca aaa gat tac att att gac cct cgg gag aat att gta atc cag 315  
35 Ser Pro Lys Asp Tyr Ile Ile Asp Pro Arg Glu Asn Ile Val Ile Gln  
36 50 55 60  
37 tgt gaa gcc aaa ggg aaa ccg ccc cca agc ttt tcc tgg acc cgt aat 363  
38 Cys Glu Ala Lys Gly Lys Pro Pro Pro Ser Phe Ser Trp Thr Arg Asn  
39 65 70 75  
40 ggg act cat ttt gac atc gat aaa gac cct ctg gtc acc atg aag cct 411  
41 Gly Thr His Phe Asp Ile Asp Lys Asp Pro Leu Val Thr Met Lys Pro  
42 80 85 90  
43 ggc aca gga acg ctc ata att aac atc atg agc gaa ggg aaa gct gag 459  
44 Gly Thr Gly Thr Leu Ile Ile Asn Ile Met Ser Glu Gly Lys Ala Glu

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45	95	100	105	110	
46	acc tat gaa gga gtc	tat cag tgt aca gca agg aac gaa cgc gga gct	507		
47	Thr Tyr Glu Gly Val	Tyr Gln Cys Thr Ala Arg Asn Glu Arg Gly Ala			
48		115	120	125	
49	gca gtt tct aat aac att gtt gtc cgc cca tcc aga tca cca ttg tgg	555			
50	Ala Val Ser Asn Asn Ile Val Val Arg Pro Ser Arg Ser Pro Leu Trp				
51		130	135	140	
52	acc aaa gaa aaa ctt gaa cca atc aca ctt caa agt ggt cag tct tta	603			
53	Thr Lys Glu Lys Leu Glu Pro Ile Thr Leu Gln Ser Gly Gln Ser Leu				
54		145	150	155	
55	gta ctt ccc tgc aga ccc cca att gga tta cca cca cct ata ata ttt	651			
56	Val Leu Pro Cys Arg Pro Pro Ile Gly Leu Pro Pro Pro Ile Ile Phe				
57		160	165	170	
58	tgg atg gat aat tcc ttt caa aga ctt cca caa agt gag aga gtt tct	699			
59	Trp Met Asp Asn Ser Phe Gln Arg Leu Pro Gln Ser Glu Arg Val Ser				
60		175	180	185	190
61	caa ggt ttg aat ggg gac ctt tat ttt tcc aat gtc ctc cca gag gac	747			
62	Gln Gly Leu Asn Gly Asp Leu Tyr Phe Ser Asn Val Leu Pro Glu Asp				
63		195	200	205	
64	acc cgc gaa gac tat atc tgt tat gct aga ttt aat cat act caa acc	795			
65	Thr Arg Glu Asp Tyr Ile Cys Tyr Ala Arg Phe Asn His Thr Gln Thr				
66		210	215	220	
67	ata cag cag aag caa cct att tct gtg aag gtg att tca gtg gat gaa	843			
68	Ile Gln Gln Lys Gln Pro Ile Ser Val Lys Val Ile Ser Val Asp Glu				
69		225	230	235	
70	ttg aat gac act ata gct gct aat ttg agt gac act gag ttt tat ggt	891			
71	Leu Asn Asp Thr Ile Ala Ala Asn Leu Ser Asp Thr Glu Phe Tyr Gly				
72		240	245	250	
73	gct aaa tca agt aga gag agg cca cca aca ttt tta act cca gaa ggc	939			
74	Ala Lys Ser Ser Arg Glu Arg Pro Pro Thr Phe Leu Thr Pro Glu Gly				
75		255	260	265	270
76	aat gca agt aac aaa gag gaa tta aga gga aat gtg ctt tca ctg gag	987			
77	Asn Ala Ser Asn Lys Glu Glu Leu Arg Gly Asn Val Leu Ser Leu Glu				
78		275	280	285	
79	tgc att gca gaa gga ctg cct acc cca att att tac tgg gca aag gaa	1035			
80	Cys Ile Ala Glu Gly Leu Pro Thr Pro Ile Ile Tyr Trp Ala Lys Glu				
81		290	295	300	
82	gat gga atg cta ccc aaa aac agg aca gtt tat aag aac ttt gag aaa	1083			
83	Asp Gly Met Leu Pro Lys Asn Arg Thr Val Tyr Lys Asn Phe Glu Lys				
84		305	310	315	
85	acc ttg cag atc att cat gtt tca gaa gca gac tct gga aat tac caa	1131			
86	Thr Leu Gln Ile Ile His Val Ser Glu Ala Asp Ser Gly Asn Tyr Gln				
87		320	325	330	
88	tgt ata gca aaa aat gca tta gga gcc atc cac cat acc att tct gtt	1179			
89	Cys Ile Ala Lys Asn Ala Leu Gly Ala Ile His His Thr Ile Ser Val				
90		335	340	345	350
91	aga gtt aaa gcg gct cca tac tgg atc aca gcc cct caa aat ctt gtg	1227			
92	Arg Val Lys Ala Ala Pro Tyr Trp Ile Thr Ala Pro Gln Asn Leu Val				
93		355	360	365	
94	ctg tcc cca gga gag gat ggg acc ttg atc tgc aga gct aat ggc aac	1275			

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95	Leu Ser Pro Gly Glu Asp Gly Thr Leu Ile Cys Arg Ala Asn Gly Asn	
96		370 375 380
97	ccc aaa ccc aga att agc tgg tta aca aat gga gtc cca ata gaa att	1323
98	Pro Lys Pro Arg Ile Ser Trp Leu Thr Asn Gly Val Pro Ile Glu Ile	
99		385 390 395
100	gcc cct gat gac ccc agc aga aaa ata gat ggc gat acc att att ttt	1371
101	Ala Pro Asp Asp Pro Ser Arg Lys Ile Asp Gly Asp Thr Ile Ile Phe	
102		400 405 410
103	tca aat gtt caa gaa aga tca agt gca gta tat cag tgc aat gcc tct	1419
104	Ser Asn Val Gln Glu Arg Ser Ser Ala Val Tyr Gln Cys Asn Ala Ser	
105		415 420 425 430
106	aat gaa tat gga tat tta ctg gca aac gca ttt gta aat gtg ctg gct	1467
107	Asn Glu Tyr Gly Tyr Leu Leu Ala Asn Ala Phe Val Asn Val Leu Ala	
108		435 440 445
109	gag cca cca cga atc ctc aca cct gca aac aca ctc tac cag gtc att	1515
110	Glu Pro Pro Arg Ile Leu Thr Pro Ala Asn Thr Leu Tyr Gln Val Ile	
111		450 455 460
112	gca aac agg cct gct tta cta gac tgt gcc ttc ttt ggg tct cct ctc	1563
113	Ala Asn Arg Pro Ala Leu Leu Asp Cys Ala Phe Phe Gly Ser Pro Leu	
114		465 470 475
115	cca acc atc gag tgg ttt aaa gga gct aaa gga agt gct ctt cat gaa	1611
116	Pro Thr Ile Glu Trp Phe Lys Gly Ala Lys Gly Ser Ala Leu His Glu	
117		480 485 490
118	gat att tat gtt tta cat gaa aat gga act ttg gaa atc aaa gat gct	1659
119	Asp Ile Tyr Val Leu His Glu Asn Gly Thr Leu Glu Ile Lys Asp Ala	
120		495 500 505 510
121	aca tgg atc gtt aaa gaa att cct gtg gcc caa aag gac agt aca gga	1707
122	Thr Trp Ile Val Lys Glu Ile Pro Val Ala Gln Lys Asp Ser Thr Gly	
123		515 520 525
124	act tat acg tgt gtt gca agg aat aaa tta ggg atg gca aag aat gaa	1755
125	Thr Tyr Thr Cys Val Ala Arg Asn Lys Leu Gly Met Ala Lys Asn Glu	
126		530 535 540
127	gtt cac tta cag ccc gaa tat gca gtt gtg caa aga ggg agc atg gtg	1803
128	Val His Leu Gln Pro Glu Tyr Ala Val Val Gln Arg Gly Ser Met Val	
129		545 550 555
130	tcc ttt gaa tgc aaa gtg aaa cat gat cac acc tta tcc ctc act gtc	1851
131	Ser Phe Glu Cys Lys Val Lys His Asp His Thr Leu Ser Leu Thr Val	
132		560 565 570
133	ctg tgg ctg aag gac aac agg gaa ctg ccc agt gat gaa agg ttc act	1899
134	Leu Trp Leu Lys Asp Asn Arg Glu Leu Pro Ser Asp Glu Arg Phe Thr	
135		575 580 585 590
136	gtt gac aag gat cat cta gtg gta gct gat gtc agt gac gat gac agc	1947
137	Val Asp Lys Asp His Leu Val Val Ala Asp Val Ser Asp Asp Asp Ser	
138		595 600 605
139	ggg acc tac acg tgt gtg gcc aac acc act ctg gac agc gtc tcc gcc	1995
140	Gly Thr Tyr Thr Cys Val Ala Asn Thr Thr Leu Asp Ser Val Ser Ala	
141		610 615 620
142	agc gct gtg ctt agc gtt gtt gct cct act cca act cca gct ccc gtt	2043
143	Ser Ala Val Leu Ser Val Val Ala Pro Thr Pro Thr Pro Ala Pro Val	
144		625 630 635

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145	tac gat gtc cca aat cct ccc ttt gac tta gaa ctg aca gat caa ctt	2091
146	Tyr Asp Val Pro Asn Pro Pro Phe Asp Leu Glu Leu Thr Asp Gln Leu	
147	640 645 650	
148	gac aaa agt gtt cag ctg tca tgg acc cca ggc gat gac aac aat agc	2139
149	Asp Lys Ser Val Gln Leu Ser Trp Thr Pro Gly Asp Asp Asn Asn Ser	
150	655 660 665 670	
151	ccc att aca aaa ttc atc atc gaa tat gaa gat gca atg cac aag cca	2187
152	Pro Ile Thr Lys Phe Ile Ile Glu Tyr Glu Asp Ala Met His Lys Pro	
153	675 680 685	
154	ggg ctg tgg cac cac caa act gaa gtt tct gga aca cag acc aca gcc	2235
155	Gly Leu Trp His His Gln Thr Glu Val Ser Gly Thr Gln Thr Thr Ala	
156	690 695 700	
157	cag ctg aag ctg tct cct tac gtg aac tac tcc ttc cgc gtg atg gca	2283
158	Gln Leu Lys Leu Ser Pro Tyr Val Asn Tyr Ser Phe Arg Val Met Ala	
159	705 710 715	
160	gtg aac agc att ggg aag agc ttg ccc agc gag gcg tct gag cag tat	2331
161	Val Asn Ser Ile Gly Lys Ser Leu Pro Ser Glu Ala Ser Glu Gln Tyr	
162	720 725 730	
163	ttg acg aaa gcc tca gaa cca gat aaa aac ccc aca gct gtg gaa gga	2379
164	Leu Thr Lys Ala Ser Glu Pro Asp Lys Asn Pro Thr Ala Val Glu Gly	
165	735 740 745 750	
166	ctg gga tca gag cct gat aat ttg gag att acg tgg aag ccc ttg aat	2427
167	Leu Gly Ser Glu Pro Asp Asn Leu Glu Ile Thr Trp Lys Pro Leu Asn	
168	755 760 765	
169	ggt ttc gaa tct aat ggg cca ggc ctt cag tac aaa gtt agc tgg cgc	2475
170	Gly Phe Glu Ser Asn Gly Pro Gly Leu Gln Tyr Lys Val Ser Trp Arg	
171	770 775 780	
172	cag aaa gat ggt gat gat gaa tgg aca tct gtg gtt gtg gca aat gta	2523
173	Gln Lys Asp Gly Asp Asp Glu Trp Thr Ser Val Val Val Ala Asn Val	
174	785 790 795	
175	tcc aaa tat att gtc tca ggc acg cca acc ttt gtt cca tac ctg atc	2571
176	Ser Lys Tyr Ile Val Ser Gly Thr Pro Thr Phe Val Pro Tyr Leu Ile	
177	800 805 810	
178	aaa gtt cag gcc ctg aat gac atg ggg ttt gcc ccc gag cca gct gta	2619
179	Lys Val Gln Ala Leu Asn Asp Met Gly Phe Ala Pro Glu Pro Ala Val	
180	815 820 825 830	
181	gtc atg gga cat tct gga gaa gac ctc cca atg gtg gct cct ggg aac	2667
182	Val Met Gly His Ser Gly Glu Asp Leu Pro Met Val Ala Pro Gly Asn	
183	835 840 845	
184	gtg cgt gtg aat gtg gtg aac agt acc tta gcc gag gtg cac tgg gac	2715
185	Val Arg Val Asn Val Val Asn Ser Thr Leu Ala Glu Val His Trp Asp	
186	850 855 860	
187	cca gta cct ctg aaa agc atc cga gga cac cta caa ggc tat cgg att	2763
188	Pro Val Pro Leu Lys Ser Ile Arg Gly His Leu Gln Gly Tyr Arg Ile	
189	865 870 875	
190	tac tat tgg aag acc cag agt tca tct aaa aga aac aga cgt cac att	2811
191	Tyr Tyr Trp Lys Thr Gln Ser Ser Ser Lys Arg Asn Arg Arg His Ile	
192	880 885 890	
193	gag aaa aag atc ctc acc ttc caa ggc agc aag act cat ggc atg ttg	2859
194	Glu Lys Lys Ile Leu Thr Phe Gln Gly Ser Lys Thr His Gly Met Leu	

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195	895	900	905	910	
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197	Pro Gly Leu Glu Pro Phe Ser His Tyr Thr Leu Asn Val Arg Val Val				
198	915	920	925		
199	aat ggg aaa ggg gag ggc cca gcc agc cct gac aga gtc ttt aat act	2955			
200	Asn Gly Lys Gly Glu Gly Pro Ala Ser Pro Asp Arg Val Phe Asn Thr				
201	930	935	940		
202	cca gaa gga gtc ccc agt gct ccc tcg tct ttg aag att gtg aat cca	3003			
203	Pro Glu Gly Val Pro Ser Ala Pro Ser Ser Leu Lys Ile Val Asn Pro				
204	945	950	955		
205	aca ctg gac tct ctc act ttg gaa tgg gat cca ccg agc cac ccg aat	3051			
206	Thr Leu Asp Ser Leu Thr Leu Glu Trp Asp Pro Pro Ser His Pro Asn				
207	960	965	970		
208	ggc att ttg aca gag tac acc tta aag tat cag cca att aac agc aca	3099			
209	Gly Ile Leu Thr Glu Tyr Thr Leu Lys Tyr Gln Pro Ile Asn Ser Thr				
210	975	980	985	990	
211	cat gaa tta ggc cct ctg gta gat ttg aaa att cct gcc aac aag aca	3147			
212	His Glu Leu Gly Pro Leu Val Asp Leu Lys Ile Pro Ala Asn Lys Thr				
213	995	1000	1005		
214	cgg tgg act tta aaa aat tta aat ttc agc act cga tat aag ttt tat	3195			
215	Arg Trp Thr Leu Lys Asn Leu Asn Phe Ser Thr Arg Tyr Lys Phe Tyr				
216	1010	1015	1020		
217	ttc tat gca caa aca tca gca gga tca gga agt caa att aca gag gaa	3243			
218	Phe Tyr Ala Gln Thr Ser Ala Gly Ser Gly Ser Gln Ile Thr Glu Glu				
219	1025	1030	1035		
220	gca gta aca act gtg gat gaa gct ggt att ctt cca cct gat gta ggt	3291			
221	Ala Val Thr Thr Val Asp Glu Ala Gly Ile Leu Pro Pro Asp Val Gly				
222	1040	1045	1050		
223	gca ggc aaa gtt caa gct gta aat acc agg atc agc aat ctt act gct	3339			
224	Ala Gly Lys Val Gln Ala Val Asn Thr Arg Ile Ser Asn Leu Thr Ala				
225	1055	1060	1065	1070	
226	gca gct gct gag acc tat gcc aat atc agt tgg gaa tat gag gga cca	3387			
227	Ala Ala Ala Glu Thr Tyr Ala Asn Ile Ser Trp Glu Tyr Glu Gly Pro				
228	1075	1080	1085		
229	gag cat gtg aac ttt tat gtt gaa tat ggt gta gca ggc agc aaa gaa	3435			
230	Glu His Val Asn Phe Tyr Val Glu Tyr Gly Val Ala Gly Ser Lys Glu				
231	1090	1095	1100		
232	gaa tgg aga aaa gaa att gta aat ggt tct cgg agc ttc ttt ggg tta	3483			
233	Glu Trp Arg Lys Glu Ile Val Asn Gly Ser Arg Ser Phe Phe Gly Leu				
234	1105	1110	1115		
235	aag ggt cta atg cca gga aca gca tac aaa gtt cga gtt ggt gct gtg	3531			
236	Lys Gly Leu Met Pro Gly Thr Ala Tyr Lys Val Arg Val Gly Ala Val				
237	1120	1125	1130		
238	ggg gac tct ggt ttt gtg agt tca gag gat gtg ttt gag aca ggc cca	3579			
239	Gly Asp Ser Gly Phe Val Ser Ser Glu Asp Val Phe Glu Thr Gly Pro				
240	1135	1140	1145	1150	
241	gcg atg gca agc cgg cag gtg gat att gca act cag ggc tgg ttc att	3627			
242	Ala Met Ala Ser Arg Gln Val Asp Ile Ala Thr Gln Gly Trp Phe Ile				
243	1155	1160	1165		
244	ggt ctg atg tgt gct gtt gct ctc ctt atc tta att ttg ctg att gtt	3675			

**Please Note:**

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

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VERIFICATION SUMMARY  
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Line	? Error/Warning	Original Text
270	W Invalid/Missing Amino Acid Numbering	1295 1300
492	W "N" or "Xaa" used: Feature required	ngctgctctc atact